Building comprehensive international datasets: Loggerhead turtles

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Review of NOAA Fisheries' Science on Marine Mammals & Turtles

Southwest and Northwest Fisheries Science Centers

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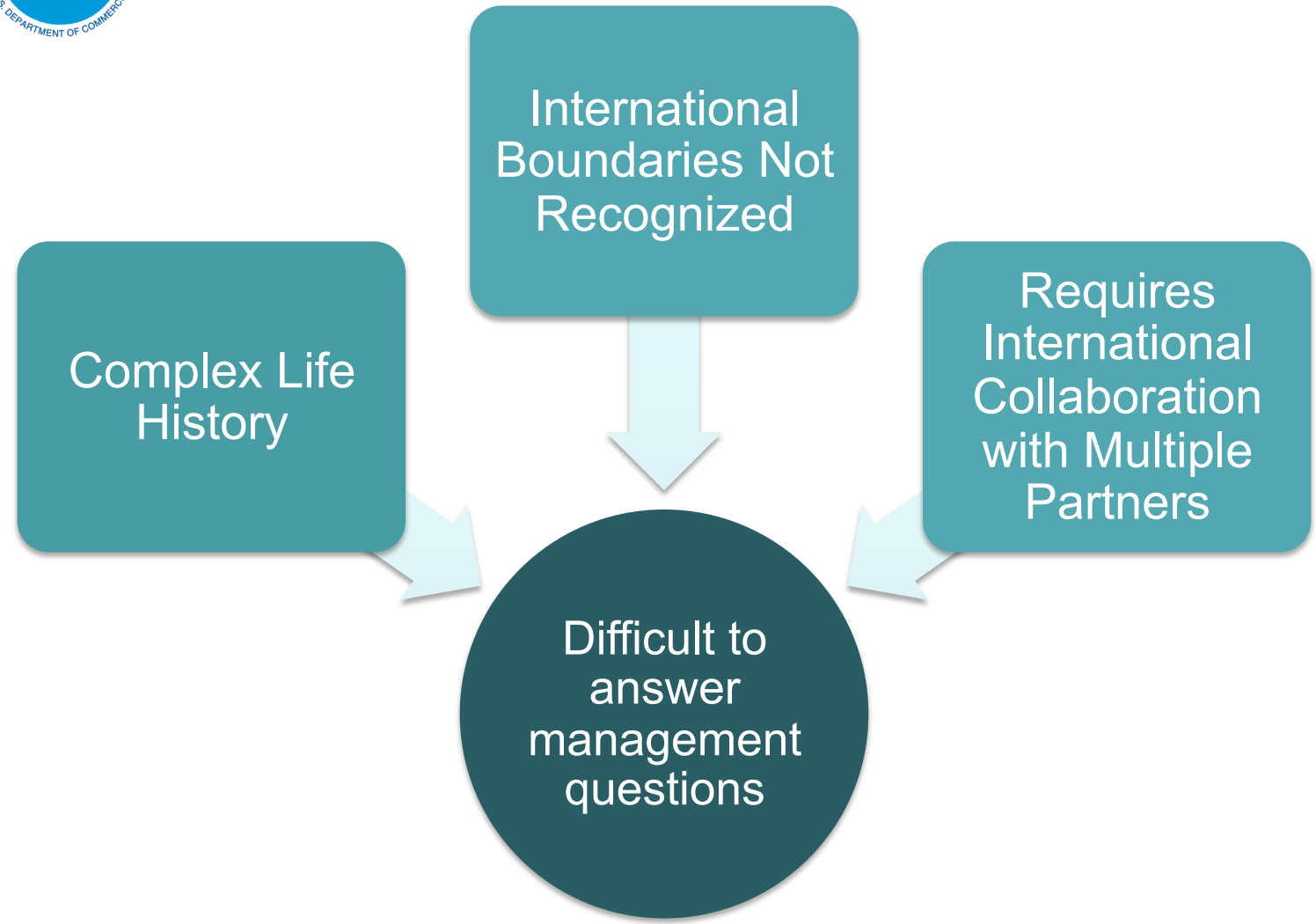
NOAA FISHERIES SERVICE

Challenges



Approach

- 7 Genetics labs (Europe, USA, Mexico, Turkey)
- Convened Atlantic-Med Loggerhead Genetics Working Group (2009-2014)
  - Data sharing agreement
  - Standardize data, analysis (800 bp mtDNA)
  - Identify and fill sampling gaps
- Define DIPs (MUs)
- Build baseline datasets for Mixed Stock Analysis

OPEN ACCESS Freely available online

PLOS | ONE

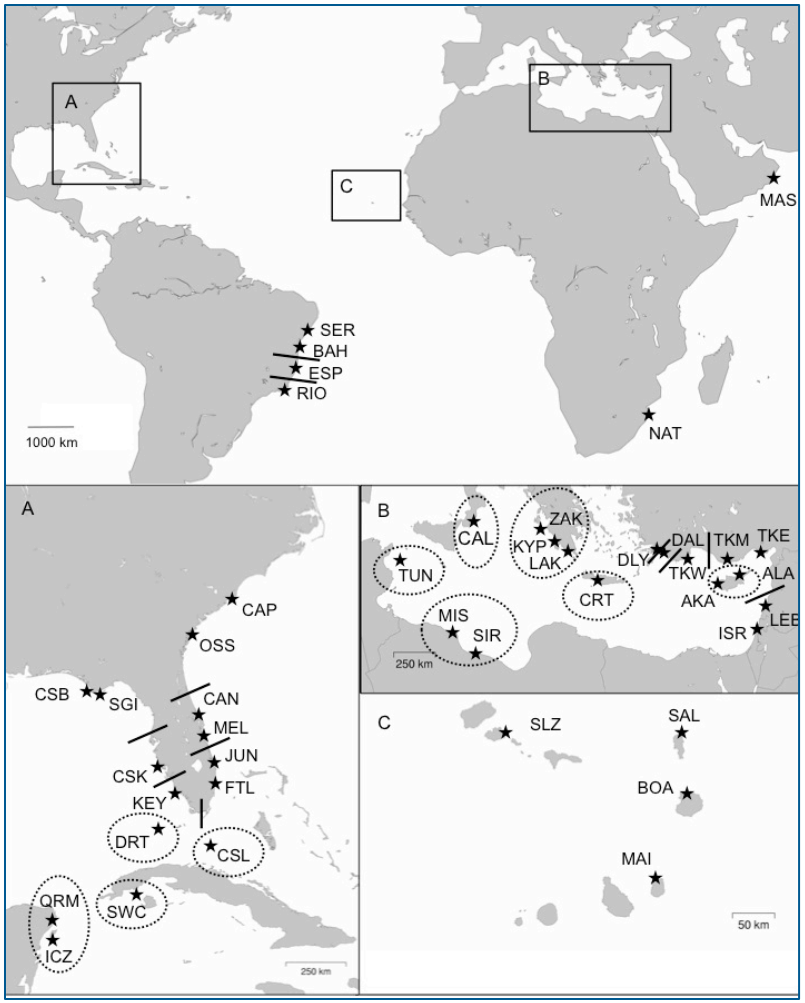
Geographic Patterns of Genetic Variation in a Broadly Distributed Marine Vertebrate: New Insights into Loggerhead Turtle Stock Structure from Expanded Mitochondrial DNA Sequences

Brian M. Shamblin[1,2], Alan B. Bolten[3], F. Alberto Abreu-Grobois[4], Karen A. Bjorndal[3], Luis Cardona[5], Carlos Carreras[5,6], Marcel Clusa[5], Catalina Monzón-Argüello[7], Campbell J. Nairn[8], Janne T. Nielsen[9], Ronel Nel[10], Luciano S. Soares[3,11], Kelly R. Stewart[2,12], Sibelle T. Vilaça[13], Oguz Türkozan[14], Can Yilmaz[14], Peter H. Dutton[2*]

"..This study represents a valuable model for conducting comprehensive international cooperative data management and research in marine ecology…."

PloSOne 9(1) 2014 e85956

Results



- mtDNA sequences from 42 rookeries (3,486 samples)
- Identified 18 DIPs (MUs)
- Baseline dataset maintained by SWFSC
- Enables meaningful Mixed Stock Analysis

Shamblin et al. 2014 PLOS ONE 9(1)

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Published online November 7

FREE ACCESS

Genetic stock composition of loggerhead turtles *Caretta caretta* bycaught in the pelagic waters of the North Atlantic

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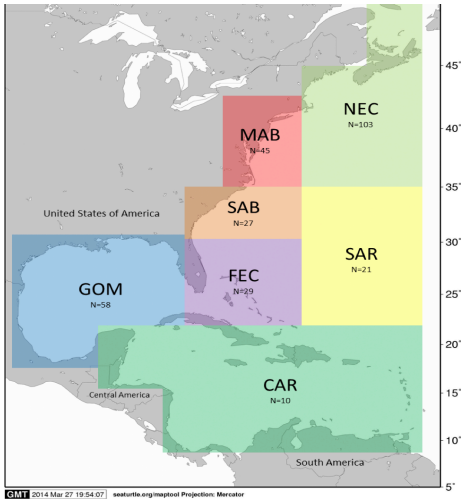
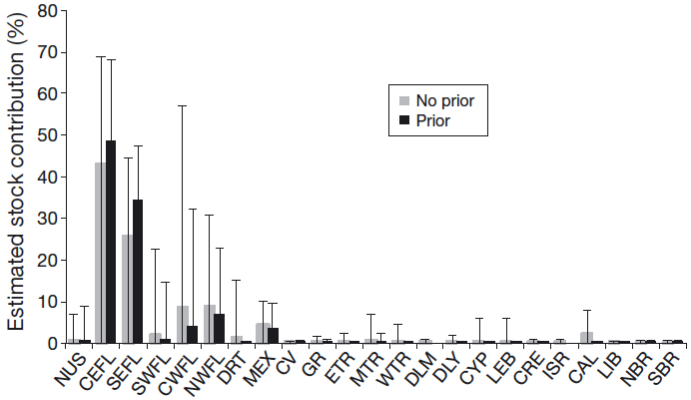
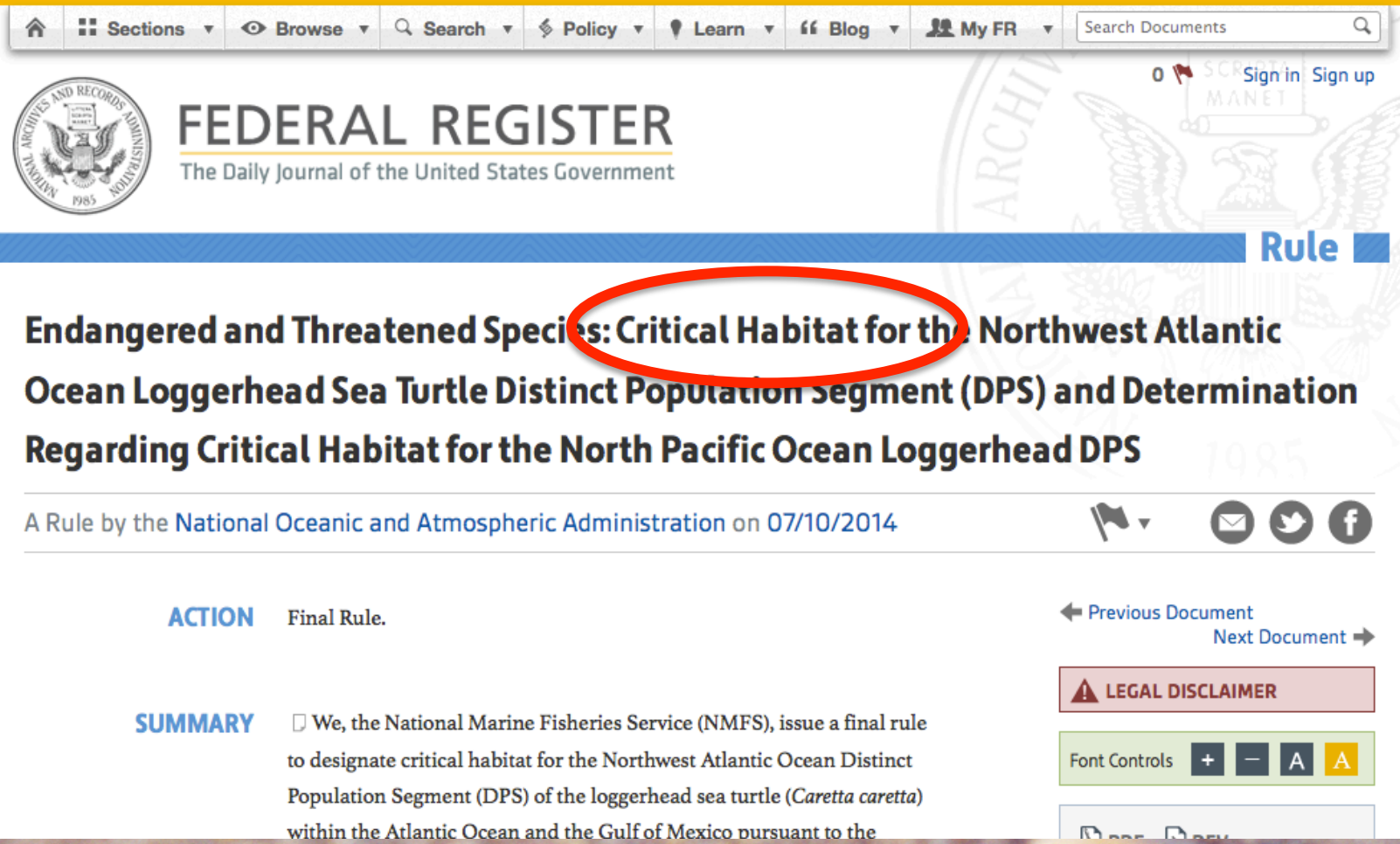




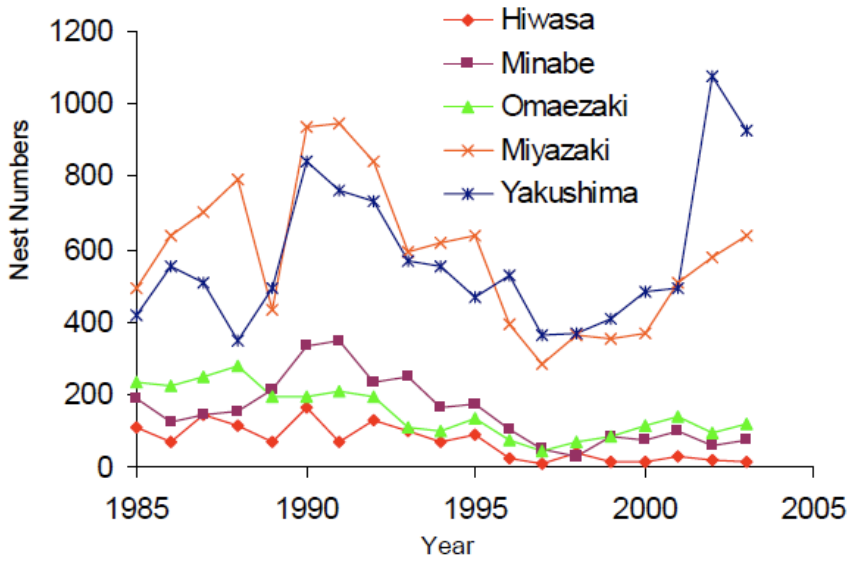
Why is this important?

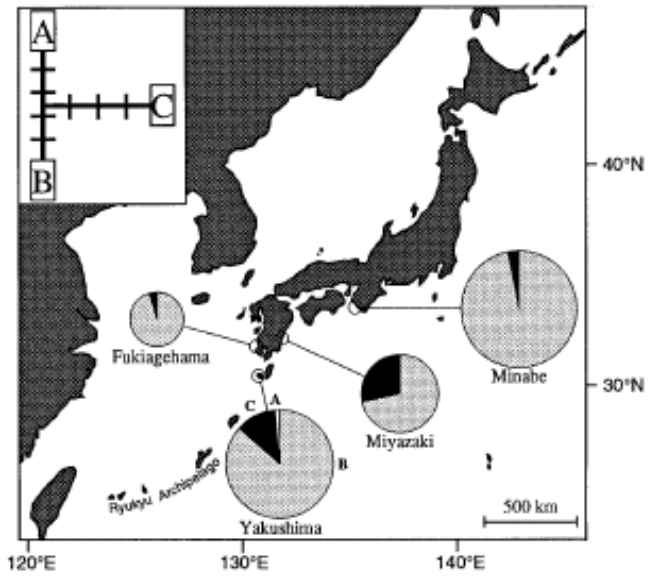


Pacific Loggerheads

Management & Conservation

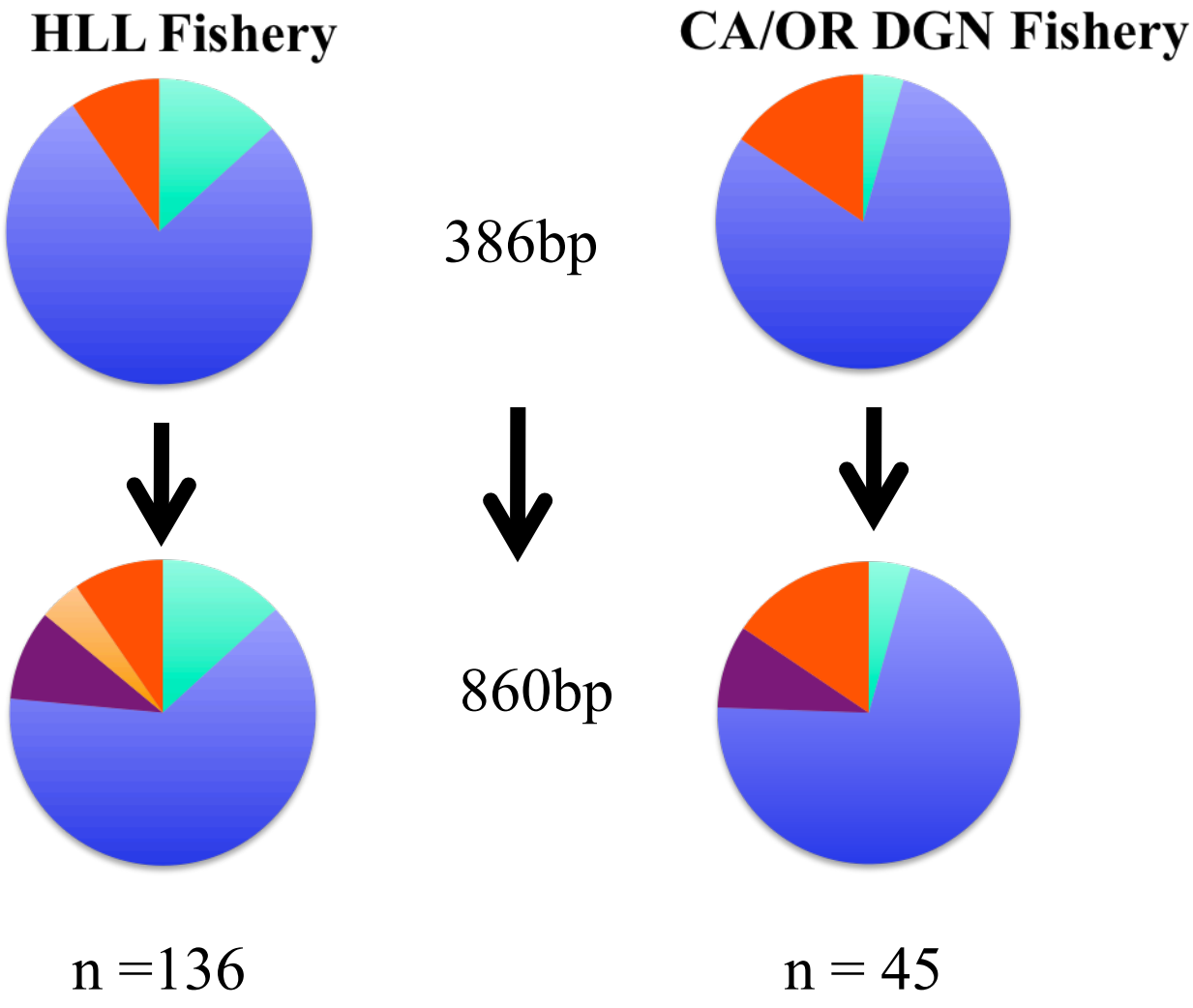
Need to identify DIPs



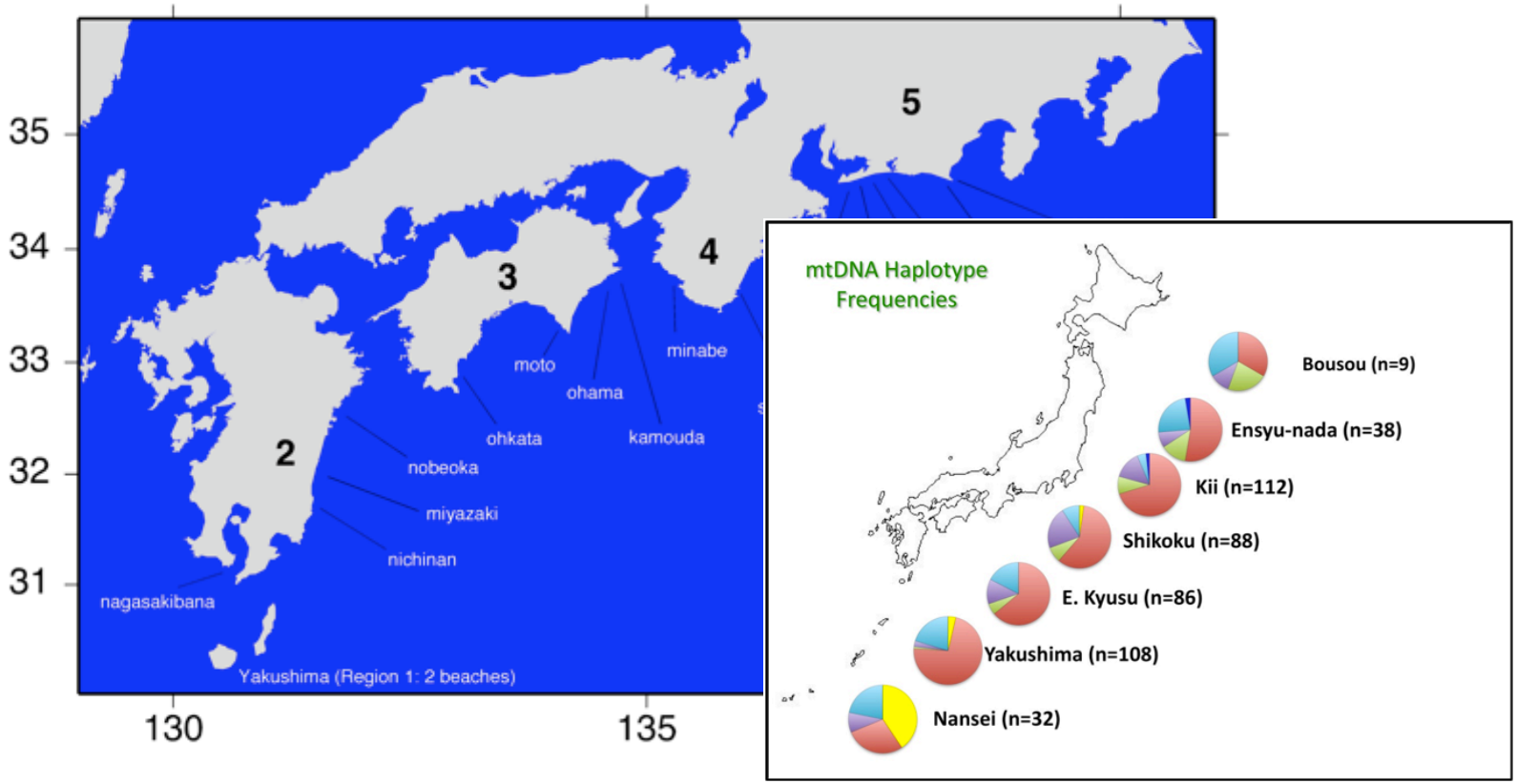


- **Can we genetically characterize DIPs?**
- **Can we assign bycatch (e.g. HLL) to source beach?**

Longer mtDNA sequences identify 3 new haplotype variants in fishery bycatch samples



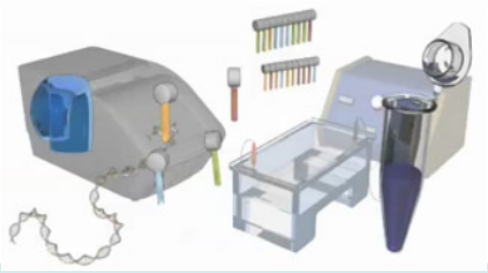
North Pacific loggerheads – toward DIPs ?

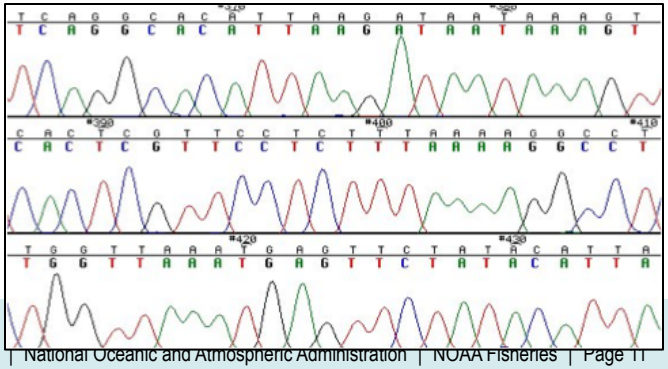


New initiative to increase sample sizes and sample all nesting populations in Japan

Strategy: Collaboration & data sharing

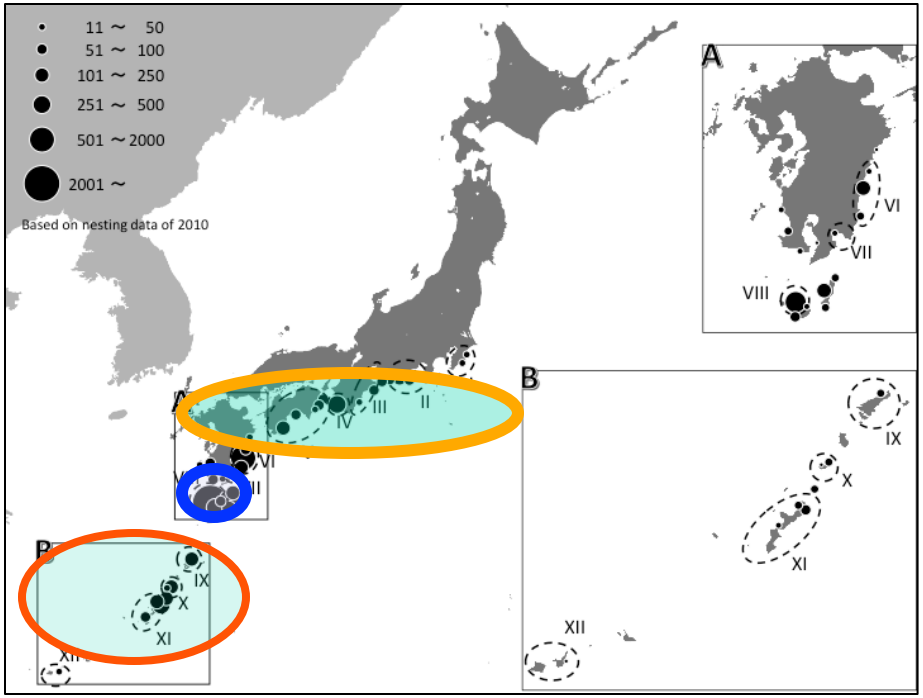
- 600 samples – 12 nesting sites in Japan
- Funded by Western Pacific Fisheries Management Council
- Primers and protocols provided by SWFSC
- Sequenced by commercial service lab in Japan
  - No CITES permits required
- Raw data sent to SWFSC for analysis
- Build baseline datasets for Mixed Stock Analysis





Fine scale genetic population structure of loggerhead turtles in the Northwest Pacific

Matsuzawa, Y., Kamezaki, N., Ishihara, T., Omuta, K., Takeshita, H., Goto, K., Arata, T., Honda, H., Kameda, K., Kashima, Y., Kayo, M., Kawazu, I., Kumazawa, Y., Kuroyanagi, K., Mizobuchi, K., Mizuno, K., Oki, K., Watanabe, K.K. , Yamamoto, A., Yamashita, Y. , Yamato, T. , Hamabata, T. , Ishizaki, A., Dutton, P.H.



3 DIPs

Ryukyu MU

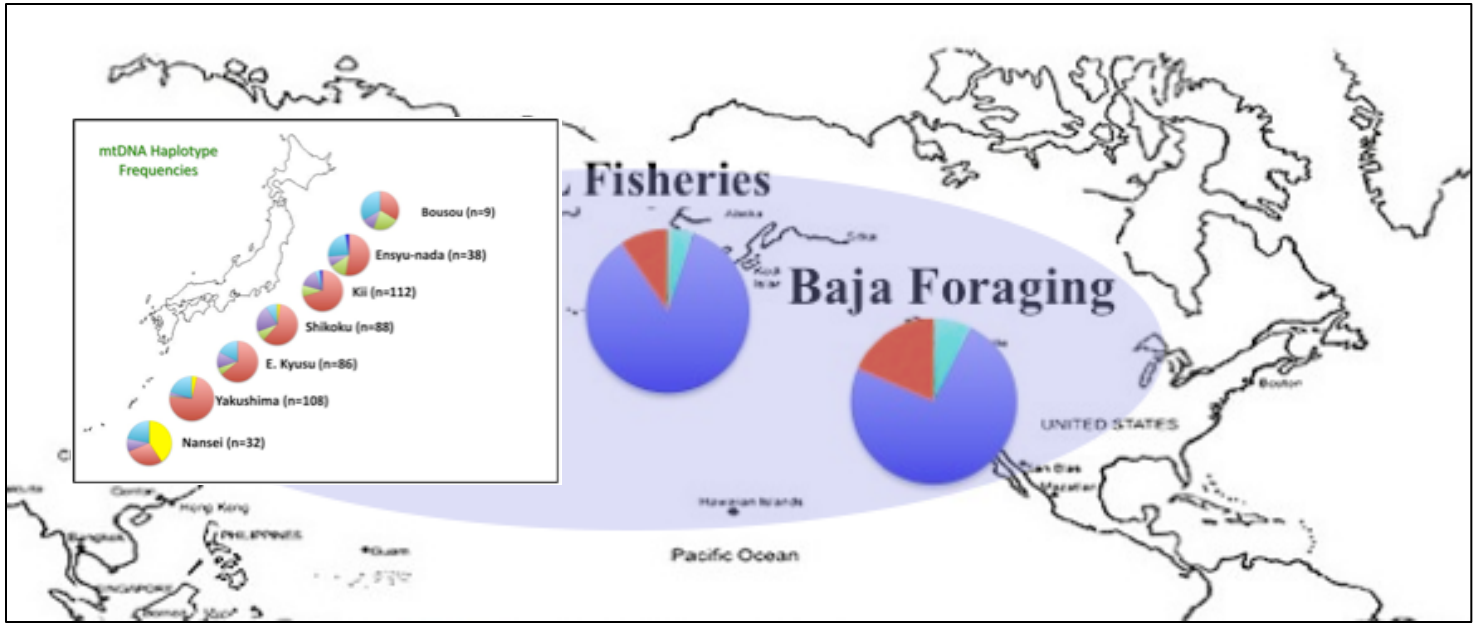
Yakushima MU

Mainland MU

760 bp mtDNA

Pacific loggerhead stock structure

Linkages w/ foraging areas



Can now carry out MSA to 3 DIPs within NW DPS

Shared databases on bycatch with Japanese working group